



Protein

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

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1: P54967 BIOTIN SYNTHASE BLINK, PubMed, Related Sequences, Taxonomy, LinkOut
(BIOTIN SYNTHETASE)

LOCUS BI0B_ARATH 378 aa PLN 01-OCT-2000
 DEFINITION BIOTIN SYNTHASE (BIOTIN SYNTHETASE).
 ACCESSION P54967
 PID g1705463
 VERSION P54967 GI:1705463
 DBSOURCE swissprot: locus BI0B_ARATH, accession P54967;
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: Oct 1, 2000.
 xrefs: gi: gi: 1045315, gi: gi: 1045316, gi: gi: 1403661, gi: gi:
1403662, gi: gi: 1769456, gi: gi: 1769457, gi: gi: 6598343, gi: gi:
2288983
 xrefs (non-sequence databases): InterPro IPR002684, Pfam PF01792
 KEYWORDS Biotin biosynthesis; Iron-sulfur; Transferase.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 1 (residues 1 to 378)
 REFERENCE
 AUTHORS Weaver, L.M., Yu, F., Wurtele, E.S. and Nikolau, B.J.
 TITLE Characterization of the cDNA and gene coding for the biotin
 synthase of *Arabidopsis thaliana*
 JOURNAL Plant Physiol. 110 (3), 1021-1028 (1996)
 MEDLINE 96417082
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. LANDSBERG ERECTA
 2 (residues 1 to 378)
 REFERENCE
 AUTHORS Patton, D., Pacella, M. and Ward, E.
 TITLE Direct Submission
 JOURNAL Submitted (??-JUL-1996)
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. COLUMBIA; TISSUE=Leaf
 3 (residues 1 to 378)
 REFERENCE
 AUTHORS Baldet, P. and Ruffet, M.L.
 TITLE Biotin synthesis in higher plants: isolation of a cDNA encoding
Arabidopsis thaliana bioB-gene product equivalent by functional
 complementation of a biotin auxotroph mutant bioB105 of *Escherichia*
coli K12
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 319 (2), 99-106 (1996)
 MEDLINE 96307524
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. COLUMBIA; TISSUE=Leaf
 4 (residues 1 to 378)
 REFERENCE
 AUTHORS Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
 Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,
 Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M.,
 Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L.,
 Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,

Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C.

TITLE Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*

JOURNAL Nature 402 (6763), 761-768 (1999)

MEDLINE 20083487

REMARK SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA

COMMENT

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[CATALYTIC ACTIVITY] DETHIOBIOTIN + (S) = BIOTIN.

[PATHWAY] LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.

[SIMILARITY] BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES FAMILY.

FEATURES

source	Location/Qualifiers 1..378 /organism="Arabidopsis thaliana" /db_xref="taxon:3702"
Protein	1..378 /product="BIOTIN SYNTHASE" /EC_number="2.8.1.6"
Site	94 /site_type="metal-binding" /note="IRON-SULFUR (POTENTIAL)."
Site	98 /site_type="metal-binding" /note="IRON-SULFUR (POTENTIAL)."
Site	101 /site_type="metal-binding" /note="IRON-SULFUR (POTENTIAL)."

ORIGIN

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121 avidaakkak eagstrfcmg aawrdtigrk tnfsqileyi keirgmgmiev cctlgmiekq
181 qalelkagl taynhnldts reyyppnvitt rsyddrletl shvrdaginv csggiiglge
241 aeedriglih tlatlpshpe svpinallav kgtpledqkp veiwemirmi gtarivmpka
301 mvrlsagrsvr fsmseqalcf lagansiftg eklltpnnd fdadqlmfkt lglipkppsf
361 seddsesenc ekvasash
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Protein

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Limits		Index	History	Clipboard			
Display	Default View	as	HTML	<input type="button" value="Save"/>	<input type="button" value="Add to Clipboard"/>		

1: CAA18303 biotin synthase (EC 2.8.1.6)
[Schizosaccharomyces pombe]

LOCUS CAA18303 363 aa **PLN** 06-APR-1999
DEFINITION biotin synthase (EC 2.8.1.6) [Schizosaccharomyces pombe].
ACCESSION CAA18303
PID g2995363
VERSION CAA18303.1 GI:2995363
DBSOURCE embl locus SPCC320, accession AL022245.2
KEYWORDS.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (residues 1 to 363)
AUTHORS Wood,V., Rajandream,M.A., Barrell,B.G., Wedler,H., Wambutt,R. and
 Wedler,E.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1998) European Schizosaccharomyces genome
 sequencing project, Sanger Centre, The Wellcome Trust Genome
 Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
 and AGOWA GmbH, Glienicker Weg 185, D-12489 Berlin, Germany
COMMENT Notes:
 Protein coding regions (CDS) have been predicted with the help of
 computer analysis using the Genefinder program in PomBase (an ACEDB
 database) with additional predictions for the branch-acceptor sites
 supplied by the program Sp3splice. CAUTION: It is possible that for
 any individual CDS we may have underestimated or overestimated the
 number of introns/exons or we may not have chosen the correct
 splice donor/acceptor sites. CDS are numbered using the following
 system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2
 (cosmid name), .01 (first CDS), c (complementary strand).
 The more significant matches with motifs in the PROSITE database
 are also included but some of these may be fortuitous. The length
 in codons is given for each CDS.
 IMPORTANT: This sequence MAY NOT be the entire insert of the
 sequenced clone. It may be shorter because we only sequence
 overlapping sections once, or longer, because we arrange for a
 small overlap between neighbouring submissions. Details of yeast
 sequencing at the Sanger Centre are available on the World Wide
 Web.
 (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
 During 1995 to 1996 about 66% of S. pombe chromosome 1 was
 sequenced by the Sanger Centre. The sequencing of the S. pombe
 genome is now being continued with funding from The European
 Commission. Fourteen European sequencing laboratories, including
 the Sanger Centre, are participating in the project.
 Cosmid c320 is overlapped by cosmid c330 at the 5' end and c1235 at
 the 3' end.
FEATURES Location/Qualifiers
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 /organism="Schizosaccharomyces pombe"

/strain="972h-"
/db_xref="taxon:4896"
/chromosome="III"
/map="IIIL"
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Protein /product="biotin synthase (EC 2.8.1.6)"
CDS 1..363
/gene="bio2"
/label=bio2
/db_xref="SPTRREMBL:O59778"
/coded_by="AL022245.2:38444..39535"
/note="SPCC320.01c, len:362"
ORIGIN
1 mftrtirqqi rrssalslvr nnwtreeiqk iydtplidli fraasihrkf hdppkvqqct
61 llsiktggct edckycaqss ryntgvkatk lmkiadevlek akiakakgst rfcmgasawrd
121 lngrnrtfkn ileiikevrs mdmevcvtlg mlneqqakel kdagltaynh nldtsreyys
181 kistrtyde rlntidnlrk aglkvcsggi lglgekkhdr vglihslatm pthpesvpfn
241 llvpiptpv gdavkerlpi hpflrsiata ricmpktiir faagrntcse seqalafmag
301 anavftgekm ltppavswds dsqlyfynwgl egmqsfeygt stegedgtft lppkerlaps
361 psl
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1: NP_011802 Biotin synthase; BLINK, PubMed, Related Sequences, Nucleotide, Genome, T
Bio2p
[Saccharomyces cerevisiae]

LOCUS NP_011802 375 aa PLN 30-JAN-2001
DEFINITION Biotin synthase; Bio2p [Saccharomyces cerevisiae].
ACCESSION NP_011802
PID g6321725
VERSION NP_011802.1 GI:6321725
DBSOURCE REFSEQ: accession NC_001139.1
KEYWORDS .
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (residues 1 to 375)
AUTHORS Goffeau,A., Barrell,B.G., Bussey,H., Davis,R.W., Dujon,B.,
Feldmann,H., Galibert,F., Hoheisel,J.D., Jacq,C., Johnston,M.,
Louis,E.J., Mewes,H.W., Murakami,Y., Philippson,P., Tettelin,H. and
Oliver,S.G.
TITLE Life with 6000 genes
JOURNAL Science 274 (5287), 546 (1996)
MEDLINE 97002444
REFERENCE 2 (residues 1 to 375)
AUTHORS Tettelin,H., Agostoni Carbone,M.L., Albermann,K., Albers,M.,
Arroyo,J., Backes,U., Barreiros,T., Bertani,I., Bjourson,A.J.,
Bruckner,M., Bruschi,C.V., Carignani,G., Castagnoli,L., Cerdan,E.,
Clemente,M.L., Coblenz,A., Coglevina,M., Coissac,E., Defoor,E.,
Del Bino,S., Delius,H., Delneri,D., de Wergifosse,P., Dujon,B.,
Kleine,K. et al.
TITLE The nucleotide sequence of *Saccharomyces cerevisiae* chromosome VII
JOURNAL Nature 387 (6632 Suppl), 81-84 (1997)
MEDLINE 97313265
REFERENCE 3 (residues 1 to 375)
AUTHORS Saccharomyces Genome Database (yeast-curator@genome.stanford.edu).
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
USA
COMMENT REFSEQ: This reference sequence was provided by the Saccharomyces
Genome Database (SGD).
Method: conceptual translation.
FEATURES Location/Qualifiers
source 1..375
/organism="Saccharomyces cerevisiae"
/strain="S288C"
/db_xref="taxon:4932"
/chromosome="VII"
Protein 1..375
/product="Biotin synthase"
/note="Bio2p"
CDS 1..375
/gene="BIO2"

/db_xref="SGD:S0003518"
/coded_by="complement(NC_001139.1:1063809..1064936)"

ORIGIN

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61 iyhtplleit haaqlqhrkw hdptkvqlct lmniksggcs edckycaqss rndtglkaek
121 mvkvdevike aeeakrngst rfclgaawrd mkgrksamkr iqemvtkvnd mgletcvtlg
181 mvdqdqakql kdagltaynh nidtsrehys kvitttrydd rlqtiknvqe sgikactggi
241 lglgeseddः igfiytlsm sphpeslpin rlvaikgtpm aeeladpksk klqfdeilrt
301 iatarivmpk aiirlaagry tmketeqfvc fmagcnsift gkkmlttmcn gwdedkamla
361 kwglqpmeaf kydrs

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